

1652

Attorney Docket No.: 13761-726

SEQUENCE LISTING #9

<110> University of Southern California
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 Chen, Dagang
 Hong, Heng
 Asward, Dana W.



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TECH CENTER 1600/2900

<120> REGULATION OF GENE EXPRESSION BY PROTEIN METHYLATION

<130> 13761-726

<140> US 09/464,377

<141> 1999-12-15

<150> US 60/112,523

<151> 1998-12-15

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3124

<212> DNA

<213> Mus musculuc

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<210> 2

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Deduced amino acid sequence of CARM1

<400> 2

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Gly Val Ala Gly Pro Gly Gly Ala Gly Pro Cys Ala Thr Val Ser Val			
20	25	30	
Phe Pro Gly Ala Arg Leu Leu Thr Ile Gly Asp Ala Asn Gly Glu Ile			
35	40	45	
Gln Arg His Ala Glu Gln Gln Ala Leu Arg Leu Glu Val Arg Ala Gly			

50	55	60
Pro	Asp	Ala Ala Gly Ile Ala Leu Tyr Ser His Glu Asp Val Cys Val
65	70	75 80
Phe	Lys Cys Ser Val Ser Arg Glu Thr Glu Cys Ser Arg Val Gly Arg	
	85	90 95
Gln	Ser Phe Ile Ile Thr Leu Gly Cys Asn Ser Val Leu Ile Gln Phe	
	100	105 110
Ala	Thr Pro His Asp Phe Cys Ser Phe Tyr Asn Ile Leu Lys Thr Cys	
	115	120 125
Arg	Gly His Thr Leu Glu Arg Ser Val Phe Ser Glu Arg Thr Glu Glu	
	130	135 140
Ser	Ser Ala Val Gln Tyr Phe Gln Phe Tyr Gly Tyr Leu Ser Gln Gln	
145	150	155 160
Gln	Asn Met Met Gln Asp Tyr Val Arg Thr Gly Thr Tyr Gln Arg Ala	
	165	170 175
Ile	Leu Gln Asn His Thr Asp Phe Lys Asp Lys Ile Val Leu Asp Val	
	180	185 190
Gly	Cys Gly Ser Gly Ile Leu Ser Phe Phe Ala Ala Gln Ala Gly Ala	
	195	200 205
Arg	Lys Ile Tyr Ala Val Glu Ala Ser Thr Met Ala Gln His Ala Glu	
	210	215 220
Val	Leu Val Lys Ser Asn Asn Leu Thr Asp Arg Ile Val Val Ile Pro	
225	230	235 240
Gly	Lys Val Glu Glu Val Ser Leu Pro Glu Gln Val Asp Ile Ile Ile	
	245	250 255
Ser	Glu Pro Met Gly Tyr Met Leu Phe Asn Glu Arg Met Leu Glu Ser	
	260	265 270
Tyr	Leu His Ala Lys Lys Tyr Leu Lys Pro Ser Gly Asn Met Phe Pro	
	275	280 285
Thr	Ile Gly Asp Val His Leu Ala Pro Phe Thr Asp Glu Gln Leu Tyr	
	290	295 300
Met	Glu Gln Phe Thr Lys Ala Asn Phe Arg Tyr Gln Pro Ser Phe His	
305	310	315 320
Gly	Val Asp Leu Ser Ala Leu Arg Gly Ala Ala Val Asp Glu Tyr Phe	
	325	330 335
Arg	Gln Pro Val Val Asp Thr Phe Asp Ile Arg Ile Leu Met Ala Lys	
	340	345 350
Ser	Val Lys Tyr Thr Val Asn Phe Leu Glu Ala Lys Glu Gly Asp Leu	
	355	360 365
His	Arg Ile Glu Ile Pro Phe Lys Phe His Met Leu His Ser Gly Leu	
	370	375 380
Val	His Gly Leu Ala Phe Trp Phe Asp Val Ala Phe Ile Gly Ser Ile	
385	390	395 400
Met	Thr Val Trp Leu Ser Thr Ala Pro Thr Glu Pro Leu Thr His Trp	
	405	410 415
Tyr	Gln Val Arg Cys Leu Phe Gln Ser Pro Leu Phe Ala Lys Ala Gly	
	420	425 430
Asp	Thr Leu Ser Gly Thr Cys Leu Leu Ile Ala Asn Lys Arg Gln Ser	
	435	440 445
Tyr	Asp Ile Ser Ile Val Ala Gln Val Asp Gln Thr Gly Ser Lys Ser	

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450	455	460													
Ser	Asn	Leu	Leu	Asp	Leu	Lys	Asn	Pro	Phe	Phe	Arg	Tyr	Thr	Gly	Thr
465					470				475					480	
Thr	Pro	Ser	Pro	Pro	Pro	Gly	Ser	His	Tyr	Thr	Ser	Pro	Ser	Glu	Asn
						485			490					495	
Met	Trp	Asn	Thr	Gly	Ser	Thr	Tyr	Asn	Leu	Ser	Ser	Gly	Val	Ala	Val
						500			505				510		
Ala	Gly	Met	Pro	Thr	Ala	Tyr	Asp	Leu	Ser	Ser	Val	Ile	Ala	Gly	Gly
						515			520				525		
Ser	Ser	Val	Gly	His	Asn	Asn	Leu	Ile	Pro	Leu	Ala	Asn	Thr	Gly	Ile
						530			535				540		
Val	Asn	His	Thr	His	Ser	Arg	Met	Gly	Ser	Ile	Met	Ser	Thr	Gly	Ile
545						550				555				560	
Val	Gln	Gly	Ser	Ser	Gly	Ala	Gln	Gly	Gly	Gly	Ser	Ser	Ser	Ala	
						565			570				575		
His	Tyr	Ala	Val	Asn	Asn	Gln	Phe	Thr	Met	Gly	Gly	Pro	Ala	Ile	Ser
						580			585				590		
Met	Ala	Ser	Pro	Met	Ser	Ile	Pro	Thr	Asn	Thr	Met	His	Tyr	Gly	Ser
						595			600				605		

<210> 3

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> CARM1 VLD TO AAA Variant

<400> 3

Met	Ala	Ala	Ala	Ala	Ala	Thr	Ala	Val	Gly	Pro	Gly	Ala	Gly	Ser	Ala
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Gly	Val	Ala	Gly	Pro	Gly	Gly	Ala	Gly	Pro	Cys	Ala	Thr	Val	Ser	Val
						20			25					30	
Phe	Pro	Gly	Ala	Arg	Leu	Leu	Thr	Ile	Gly	Asp	Ala	Asn	Gly	Glu	Ile
						35			40					45	
Gln	Arg	His	Ala	Glu	Gln	Gln	Ala	Leu	Arg	Leu	Glu	Val	Arg	Ala	Gly
						50			55					60	
Pro	Asp	Ala	Ala	Gly	Ile	Ala	Leu	Tyr	Ser	His	Glu	Asp	Val	Cys	Val
65						70				75				80	
Phe	Lys	Cys	Ser	Val	Ser	Arg	Glu	Thr	Glu	Cys	Ser	Arg	Val	Gly	Arg
						85			90					95	
Gln	Ser	Phe	Ile	Ile	Thr	Leu	Gly	Cys	Asn	Ser	Val	Leu	Ile	Gln	Phe
						100			105					110	
Ala	Thr	Pro	His	Asp	Phe	Cys	Ser	Phe	Tyr	Asn	Ile	Leu	Lys	Thr	Cys
						115			120					125	
Arg	Gly	His	Thr	Leu	Glu	Arg	Ser	Val	Phe	Ser	Glu	Arg	Thr	Glu	Glu
						130			135					140	
Ser	Ser	Ala	Val	Gln	Tyr	Phe	Gln	Phe	Tyr	Gly	Tyr	Leu	Ser	Gln	Gln
145						145			150					155	
Gln	Asn	Met	Met	Gln	Asp	Tyr	Val	Arg	Thr	Gly	Thr	Tyr	Gln	Arg	Ala

165	170	175
Ile Leu Gln Asn His Thr Asp Phe Lys	Asp Lys Ile Ala Ala Ala	Ala Val
180	185	190
Gly Cys Gly Ser Gly Ile Leu Ser Phe Phe Ala Ala Gln Ala Gly Ala		
195	200	205
Arg Lys Ile Tyr Ala Val Glu Ala Ser Thr Met Ala Gln His Ala Glu		
210	215	220
Val Leu Val Lys Ser Asn Asn Leu Thr Asp Arg Ile Val Val Ile Pro		
225	230	235
Gly Lys Val Glu Glu Val Ser Leu Pro Glu Gln Val Asp Ile Ile Ile		
245	250	255
Ser Glu Pro Met Gly Tyr Met Leu Phe Asn Glu Arg Met Leu Glu Ser		
260	265	270
Tyr Leu His Ala Lys Lys Tyr Leu Lys Pro Ser Gly Asn Met Phe Pro		
275	280	285
Thr Ile Gly Asp Val His Leu Ala Pro Phe Thr Asp Glu Gln Leu Tyr		
290	295	300
Met Glu Gln Phe Thr Lys Ala Asn Phe Arg Tyr Gln Pro Ser Phe His		
305	310	315
Gly Val Asp Leu Ser Ala Leu Arg Gly Ala Ala Val Asp Glu Tyr Phe		
325	330	335
Arg Gln Pro Val Val Asp Thr Phe Asp Ile Arg Ile Leu Met Ala Lys		
340	345	350
Ser Val Lys Tyr Thr Val Asn Phe Leu Glu Ala Lys Glu Gly Asp Leu		
355	360	365
His Arg Ile Glu Ile Pro Phe Lys Phe His Met Leu His Ser Gly Leu		
370	375	380
Val His Gly Leu Ala Phe Trp Phe Asp Val Ala Phe Ile Gly Ser Ile		
385	390	395
Met Thr Val Trp Leu Ser Thr Ala Pro Thr Glu Pro Leu Thr His Trp		
405	410	415
Tyr Gln Val Arg Cys Leu Phe Gln Ser Pro Leu Phe Ala Lys Ala Gly		
420	425	430
Asp Thr Leu Ser Gly Thr Cys Leu Leu Ile Ala Asn Lys Arg Gln Ser		
435	440	445
Tyr Asp Ile Ser Ile Val Ala Gln Val Asp Gln Thr Gly Ser Lys Ser		
450	455	460
Ser Asn Leu Leu Asp Leu Lys Asn Pro Phe Phe Arg Tyr Thr Gly Thr		
465	470	475
Thr Pro Ser Pro Pro Gly Ser His Tyr Thr Ser Pro Ser Glu Asn		
485	490	495
Met Trp Asn Thr Gly Ser Thr Tyr Asn Leu Ser Ser Gly Val Ala Val		
500	505	510
Ala Gly Met Pro Thr Ala Tyr Asp Leu Ser Ser Val Ile Ala Gly Gly		
515	520	525
Ser Ser Val Gly His Asn Asn Leu Ile Pro Leu Ala Asn Thr Gly Ile		
530	535	540
Val Asn His Thr His Ser Arg Met Gly Ser Ile Met Ser Thr Gly Ile		
545	550	555
Val Gln Gly Ser Ser Gly Ala Gln Gly Gly Ser Ser Ser Ala		

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	565		570		575										
His	Tyr	Ala	Val	Asn	Asn	Gln	Phe	Thr	Met	Gly	Gly	Pro	Ala	Ile	Ser
				580				585					590		
Met	Ala	Ser	Pro	Met	Ser	Ile	Pro	Thr	Asn	Thr	Met	His	Tyr	Gly	Ser
						595			600				605		

<210> 4

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide used for in vitro methylation experiments

<400> 4

Gly	Gly	Phe	Gly	Gly	Arg	Gly	Gly	Phe	Gly
1				5				10	

<210> 5

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide used for in vitro methylation experiments

<400> 5

Gly	Gly	Phe	Gly	Gly	Lys	Gly	Gly	Phe	Gly
1				5				10	

<210> 6

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide used to generate anti-CARM1 antisera

<400> 6

Cys	Ser	Pro	Met	Ser	Ile	Pro	Thr	Asn	Thr	Met	His	Tyr	Gly	Ser
1					5				10			15		

<210> 7

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Human PRMT1

<400> 7

Met Glu Val Ser Cys Gly Gln Ala Glu Ser Ser Glu Lys Pro Asn Ala
 1 5 10 15
 Glu Asp Met Thr Ser Lys Asp Tyr Tyr Phe Asp Ser Tyr Ala His Phe
 20 25 30
 Gly Ile His Glu Glu Met Leu Lys Asp Glu Val Arg Thr Leu Thr Tyr
 35 40 45
 Arg Asn Ser Met Phe His Asn Arg His Leu Phe Lys Asp Lys Val Val
 50 55 60
 Leu Asp Val Gly Ser Gly Thr Gly Ile Leu Cys Met Phe Ala Ala Lys
 65 70 75 80
 Ala Gly Ala Arg Lys Val Ile Gly Ile Val Cys Ser Ser Ile Ser Asp
 85 90 95
 Tyr Ala Val Lys Ile Val Lys Ala Asn Lys Leu Asp His Val Val Thr
 100 105 110
 Ile Ile Lys Gly Lys Val Glu Glu Val Glu Leu Pro Val Glu Lys Val
 115 120 125
 Asp Ile Ile Ile Ser Glu Trp Met Gly Tyr Cys Leu Phe Tyr Glu Ser
 130 135 140
 Met Leu Asn Thr Val Leu Tyr Ala Arg Asp Lys Trp Leu Ala Pro Asp
 145 150 155 160
 Gly Leu Ile Phe Pro Asp Arg Ala Thr Leu Tyr Val Thr Ala Ile Glu
 165 170 175
 Asp Arg Gln Tyr Lys Asp Tyr Lys Ile His Trp Trp Glu Asn Val Tyr
 180 185 190
 Gly Phe Asp Met Ser Cys Ile Lys Asp Val Ala Ile Lys Glu Pro Leu
 195 200 205
 Val Asp Val Val Asp Pro Lys Gln Leu Val Thr Asn Ala Cys Leu Ile
 210 215 220
 Lys Glu Val Asp Ile Tyr Thr Val Lys Val Glu Asp Leu Thr Phe Thr
 225 230 235 240
 Ser Pro Phe Cys Leu Gln Val Lys Arg Asn Asp Tyr Val His Ala Leu
 245 250 255
 Val Ala Tyr Phe Asn Ile Glu Phe Thr Arg Cys His Lys Arg Thr Gly
 260 265 270
 Phe Ser Thr Ser Pro Glu Ser Pro Tyr Thr His Trp Lys Gln Thr Val
 275 280 285
 Phe Tyr Met Glu Asp Tyr Leu Thr Val Lys Thr Gly Glu Glu Ile Phe
 290 295 300
 Gly Thr Ile Gly Met Arg Pro Asn Ala Lys Asn Asn Arg Asp Leu Asp
 305 310 315 320
 Phe Thr Ile Asp Leu Asp Phe Lys Gly Gln Leu Cys Glu Leu Ser Cys
 325 330 335
 Ser Thr Asp Tyr Arg Met Arg
 340

<210> 8

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> Human PRMT2

<400> 8

Met Ala Thr Ser Gly Asp Cys Pro Arg Ser Glu Ser Gln Gly Glu Glu
 1 5 10 15
 Pro Ala Glu Cys Ser Glu Ala Gly Leu Leu Gln Glu Gly Val Gln Pro
 20 25 30
 Glu Glu Phe Val Ala Ile Ala Asp Tyr Ala Ala Thr Asp Glu Thr Gln
 35 40 45
 Leu Ser Phe Leu Arg Gly Glu Lys Ile Leu Ile Leu Arg Gln Thr Thr
 50 55 60
 Ala Asp Trp Trp Trp Gly Glu Arg Ala Gly Cys Cys Gly Tyr Ile Pro
 65 70 75 80
 Ala Asn His Val Gly Lys His Val Asp Glu Tyr Asp Pro Glu Asp Thr
 85 90 95
 Trp Gln Asp Glu Glu Tyr Phe Gly Ser Tyr Gly Thr Leu Lys Leu His
 100 105 110
 Leu Glu Met Leu Ala Asp Gln Pro Arg Thr Thr Lys Tyr His Ser Val
 115 120 125
 Ile Leu Gln Asn Lys Glu Ser Leu Thr Asp Lys Val Ile Leu Asp Val
 130 135 140
 Gly Cys Gly Thr Gly Ile Ile Ser Leu Phe Cys Ala His Tyr Ala Arg
 145 150 155 160
 Pro Arg Ala Val Tyr Ala Val Glu Ala Ser Glu Met Ala Gln His Thr
 165 170 175
 Gly Gln Leu Val Leu Gln Asn Gly Phe Ala Asp Ile Ile Thr Val Tyr
 180 185 190
 Gln Gln Lys Val Glu Asp Val Val Leu Pro Glu Lys Val Asp Val Leu
 195 200 205
 Val Ser Glu Trp Met Gly Thr Cys Leu Leu Phe Glu Phe Met Ile Glu
 210 215 220
 Ser Ile Leu Tyr Ala Arg Asp Ala Trp Leu Lys Glu Asp Gly Val Ile
 225 230 235 240
 Trp Pro Thr Met Ala Ala Leu His Leu Val Pro Cys Ser Ala Asp Lys
 245 250 255
 Asp Tyr Arg Ser Lys Val Leu Phe Trp Asp Asn Ala Tyr Glu Phe Asn
 260 265 270
 Leu Ser Ala Leu Lys Ser Leu Ala Val Lys Glu Phe Phe Ser Lys Pro
 275 280 285
 Lys Tyr Asn His Ile Leu Lys Pro Glu Asp Cys Leu Ser Glu Pro Cys
 290 295 300
 Thr Ile Leu Gln Leu Asp Met Arg Thr Val Gln Ile Ser Asp Leu Glu
 305 310 315 320
 Thr Leu Arg Gly Glu Leu Arg Phe Asp Ile Arg Lys Ala Gly Thr Leu
 325 330 335
 His Gly Phe Thr Ala Trp Phe Ser Val His Phe Gln Ser Leu Gln Glu
 340 345 350
 Gly Gln Pro Pro Gln Val Leu Ser Thr Gly Pro Phe His Pro Thr Thr

355	360	365	
His Trp Lys Gln Thr Leu Phe Met Met Asp Asp Pro Val Pro Val His			
370	375	380	
Thr Gly Asp Val Val Thr Gly Ser Val Val Leu Gln Arg Asn Pro Val			
385	390	395	400
Trp Arg Arg His Met Ser Val Ala Leu Ser Trp Ala Val Thr Ser Arg			
405	410	415	
Gln Asp Pro Thr Ser Gln Lys Val Gly Glu Lys Val Phe Pro Ile Trp			
420	425	430	

Arg

<210> 9
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> Human PRMT3

<400> 9

Asp Glu Pro Glu Leu Ser Asp Ser Gly Asp Glu Ala Ala Trp Glu Asp			
1	5	10	15
Glu Asp Asp Ala Asp Leu Pro His Gly Lys Gln Gln Thr Pro Cys Leu			
20	25	30	
Phe Cys Asn Arg Leu Phe Thr Ser Ala Glu Glu Thr Phe Ser His Cys			
35	40	45	
Lys Ser Glu His Gln Phe Asn Ile Asp Ser Met Val His Lys His Gly			
50	55	60	
Leu Glu Phe Tyr Gly Tyr Ile Lys Leu Ile Asn Phe Ile Arg Leu Lys			
65	70	75	80
Asn Pro Thr Val Glu Tyr Met Asn Ser Ile Tyr Asn Pro Val Pro Trp			
85	90	95	
Glu Lys Glu Glu Tyr Leu Lys Pro Val Leu Glu Asp Asp Leu Leu Leu			
100	105	110	
Gln Phe Asp Val Glu Asp Leu Tyr Glu Pro Val Ser Val Pro Phe Ser			
115	120	125	
Tyr Pro Asn Gly Leu Ser Glu Asn Thr Ser Val Val Glu Lys Leu Lys			
130	135	140	
His Met Glu Ala Arg Ala Leu Ser Ala Glu Ala Ala Leu Ala Arg Ala			
145	150	155	160
Arg Glu Asp Leu Gln Lys Met Lys Gln Phe Ala Gln Asp Phe Val Met			
165	170	175	
His Thr Asp Val Arg Thr Cys Ser Ser Ser Thr Ser Val Ile Ala Asp			
180	185	190	
Leu Gln Glu Asp Glu Asp Gly Val Tyr Phe Ser Ser Tyr Gly His Tyr			
195	200	205	
Gly Ile His Glu Glu Met Leu Lys Asp Lys Ile Arg Thr Glu Ser Tyr			
210	215	220	
Arg Asp Phe Ile Tyr Gln Asn Pro His Ile Phe Lys Asp Lys Val Val			

225	230	235	240
Leu Asp Val Gly Cys	Gly Thr Gly Ile	Leu Ser Met Phe Ala	Ala Lys
245	250	255	
Ala Gly Ala Lys Lys	Val Leu Gly Val	Asp Gln Ser Glu	Ile Leu Tyr
260	265	270	
Gln Ala Met Asp Ile Ile Arg	Leu Asn Lys	Leu Glu Asp	Thr Ile Thr
275	280	285	
Leu Ile Lys Gly Lys Ile	Glu Glu Val His	Leu Pro Val	Glu Lys Val
290	295	300	
Asp Val Ile Ile Ser	Glu Trp Met Gly	Tyr Phe Leu	Leu Phe Glu Ser
305	310	315	320
Met Leu Asp Ser Val	Leu Tyr Ala Lys	Asn Lys Tyr	Leu Ala Lys Gly
325	330	335	
Gly Ser Val Tyr Pro Asp Ile Cys	Thr Ile Ser	Leu Val Ala	Val Ser
340	345	350	
Asp Val Asn Lys His Ala Asp Arg	Ile Ala Phe Trp	Asp Asp Val	Tyr
355	360	365	
Gly Phe Lys Met Ser Cys	Met Lys Lys Ala	Val Ile Pro	Glu Ala Val
370	375	380	
Val Glu Val Leu Asp Pro	Lys Thr Leu Ile	Ser Glu Pro Cys	Gly Ile
385	390	395	400
Lys His Ile Asp Cys His	Thr Ser Ile	Ser Asp Leu Glu	Phe Ser
405	410	415	
Ser Asp Phe Thr Leu Lys Ile	Thr Arg Thr	Ser Met Cys	Thr Ala Ile
420	425	430	
Ala Gly Tyr Phe Asp Ile	Tyr Phe Glu Lys	Asn Cys His	Asn Arg Val
435	440	445	
Val Phe Ser Thr Gly Pro	Gln Ser Thr Lys	Thr His Trp	Lys Gln Thr
450	455	460	
Val Phe Leu Leu Glu Lys	Pro Phe Ser Val	Lys Ala Gly	Glu Ala Leu
465	470	475	480
Lys Gly Lys Val Thr Val	His Lys Asn Lys	Lys Asp Pro	Arg Ser Leu
485	490	495	
Thr Val Thr Leu Thr	Leu Asn Asn Ser	Thr Gln Thr	Tyr Gly Leu Gln
500	505	510	

<210> 10
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> Yeast ODP1 Protein Arginine Methyltransferase

<400> 10
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1 5 10 15
Ser Glu Ser Glu Gln His Tyr Phe Asn Ser Tyr Asp His Tyr Gly Ile
20 25 30
His Glu Glu Met Leu Gln Asp Thr Val Arg Thr Leu Ser Tyr Arg Asn

	35	40	45
Ala	Ile Ile Gln Asn Lys Asp	Leu Phe Lys Asp Lys	Ile Val Leu Asp
50	55	60	
Val	Gly Cys Gly Thr Gly	Ile Leu Ser Met Phe	Ala Ala Lys His Gly
65	70	75	80
Ala	Lys His Val Ile Gly Val Asp	Met Ser Ser Ile Ile Glu	Met Ala
	85	90	95
Lys	Glu Leu Val Glu Leu Asn Gly	Phe Ser Asp Lys Ile Thr	Leu Leu
	100	105	110
Arg	Gly Lys Leu Glu Asp Val His	Leu Pro Phe Pro Lys Val Asp Ile	
	115	120	125
Ile	Ile Ser Glu Trp Met Gly Tyr	Phe Leu Leu Tyr Glu Ser Met Met	
130	135	140	
Asp	Thr Val Leu Tyr Ala Arg Asp His	Tyr Leu Val Glu Gly	Gly Leu
145	150	155	160
Ile	Phe Pro Asp Lys Cys Ser Ile His	Leu Ala Gly Leu Glu Asp Ser	
	165	170	175
Gln	Tyr Lys Asp Glu Lys Leu Asn Tyr	Trp Gln Asp Val Tyr Gly Phe	
	180	185	190
Asp	Tyr Ser Pro Phe Val Pro Leu Val	Leu His Glu Pro Ile Val Asp	
	195	200	205
Thr	Val Glu Arg Asn Asn Val Asn	Thr Ser Asp Lys Leu Ile Glu	
210	215	220	
Phe	Asp Leu Asn Thr Val Lys Ile Ser Asp	Leu Ala Phe Lys Ser Asn	
225	230	235	240
Phe	Lys Leu Thr Ala Lys Arg Gln Asp	Met Ile Asn Gly Ile Val Thr	
	245	250	255
Trp	Phe Asp Ile Val Phe Pro Ala Pro	Lys Gly Lys Arg Pro Val Glu	
	260	265	270
Phe	Ser Thr Gly Pro His Ala Pro	Tyr Thr His Trp Lys Gln Thr Ile	
	275	280	285
Phe	Tyr Phe Pro Asp Asp Leu Asp Ala Glu	Thr Gly Asp Thr Ile Glu	
	290	295	300
Gly	Glu Leu Val Cys Ser Pro Asn Glu Lys	Asn Asn Arg Asp Leu Asn	
305	310	315	320
Ile	Lys Ile Ser Tyr Lys Phe Glu Ser Asn	Gly Ile Asp Gly Asn Ser	
	325	330	335
Arg	Ser Arg Lys Asn Glu Gly Ser	Tyr Leu Met His	
	340	345	